

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: ASTRA AB
- (B) STREET: Västra Mälarehamnen 9
- (C) CITY: Södertälje
- (E) COUNTRY: Sweden
- (F) POSTAL CODE (ZIP): S-151 85
- (G) TELEPHONE: +46-8-553 260 00
- (H) TELEFAX: +46-8-553 288 20
- (I) TELEX: 19237 astra s

(ii) TITLE OF INVENTION: DNA Sequences for Expression of Polypeptides

(iii) NUMBER OF SEQUENCES: 4

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release =1.0, Version =1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2428 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (F) TISSUE TYPE: mammary gland

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 82..2319
- (D) OTHER INFORMATION: /product= "bile-salt-stimulated lipase"

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 985..1173

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 1174..1377

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 1378..1575

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 1576..2415

- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION:151..2316
- (ix) FEATURE:
 - (A) NAME/KEY: polyA_signal
 - (B) LOCATION:2397..2402
- (ix) FEATURE:
 - (A) NAME/KEY: repeat_region
 - (B) LOCATION:1756..2283
- (ix) FEATURE:
 - (A) NAME/KEY: 5'UTR
 - (B) LOCATION:1..81
- (ix) FEATURE:
 - (A) NAME/KEY: repeat_unit
 - (B) LOCATION:1756..1788
- (ix) FEATURE:
 - (A) NAME/KEY: repeat_unit
 - (B) LOCATION:1789..1821
- (ix) FEATURE:
 - (A) NAME/KEY: repeat_unit
 - (B) LOCATION:1822..1854
- (ix) FEATURE:
 - (A) NAME/KEY: repeat_unit
 - (B) LOCATION:1855..1887
- (ix) FEATURE:
 - (A) NAME/KEY: repeat_unit
 - (B) LOCATION:1888..1920
- (ix) FEATURE:
 - (A) NAME/KEY: repeat_unit
 - (B) LOCATION:1921..1953
- (ix) FEATURE:
 - (A) NAME/KEY: repeat_unit
 - (B) LOCATION:1954..1986
- (ix) FEATURE:
 - (A) NAME/KEY: repeat_unit
 - (B) LOCATION:1987..2019
- (ix) FEATURE:
 - (A) NAME/KEY: repeat_unit
 - (B) LOCATION:2020..2052
- (ix) FEATURE:
 - (A) NAME/KEY: repeat_unit
 - (B) LOCATION:2053..2085
- (ix) FEATURE:
 - (A) NAME/KEY: repeat_unit
 - (B) LOCATION:2086..2118
- (ix) FEATURE:
 - (A) NAME/KEY: repeat_unit
 - (B) LOCATION:2119..2151
- (ix) FEATURE:
 - (A) NAME/KEY: repeat_unit
 - (B) LOCATION:2152..2184

(ix) FEATURE:

(A) NAME/KEY: repeat_unit
(B) LOCATION:2185..2217

(ix) FEATURE:

(A) NAME/KEY: repeat_unit
(B) LOCATION:2218..2250

(ix) FEATURE:

(A) NAME/KEY: repeat_unit
(B) LOCATION:2251..2283

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Nilsson, Jeanette
Bläckberg, Lars
Carlsson, Peter
Enerbäck, Sven
Hernell, Olle
Bjursell, Gunnar

(B) TITLE: cDNA cloning of human-milk
bile-salt-stimulated lipase and evidence for its
identity to pancreatic carboxylic ester hydrolase

(C) JOURNAL: Eur. J. Biochem.

(D) VOLUME: 192

(F) PAGES: 543-550

(G) DATE: Sept.-1990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ACCTTCTGTA TCAGTTAAGT GTCAAGATGG AAGGAACAGC AGTCTCAAGA TAATGCAAAG	60
AGTTTATTCA TCCAGAGGCT G ATG CTC ACC ATG GGG CGC CTG CAA CTG GTT	111
Met Leu Thr Met Gly Arg Leu Gln Leu Val	
-23 -20 -15	
GTG TTG GGC CTC ACC TGC TGC TGG GCA GTG GCG AGT GCC GCG AAG CTG	159
Val Leu Gly Leu Thr Cys Cys Trp Ala Val Ala Ser Ala Ala Lys Leu	
-10 -5 1	
GGC GCC GTG TAC ACA GAA GGT GGG TTC GTG GAA GGC GTC AAT AAG AAG	207
Gly Ala Val Tyr Thr Glu Gly Gly Phe Val Glu Gly Val Asn Lys Lys	
5 10 15	
CTC GGC CTC CTG GGT GAC TCT GTG GAC ATC TTC AAG GGC ATC CCC TTC	255
Leu Gly Leu Leu Gly Asp Ser Val Asp Ile Phe Lys Gly Ile Pro Phe	
20 25 30 35	
GCA GCT CCC ACC AAG GCC CTG GAA AAT CCT CAG CCA CAT CCT GGC TGG	303
Ala Ala Pro Thr Lys Ala Leu Glu Asn Pro Gln Pro His Pro Gly Trp	
40 45 50	
CAA GGC ACC CTG AAG GCC AAG AAC TTC AAG AAG AGA TGC CTG CAG GCC	351
Gln Gly Thr Leu Lys Ala Lys Asn Phe Lys Lys Arg Cys Leu Gln Ala	
55 60 65	
ACC ATC ACC CAG GAC AGC ACC TAC GGG GAT GAA GAC TGC CTG TAC CTC	399
Thr Ile Thr Gln Asp Ser Thr Tyr Gly Asp Glu Asp Cys Leu Tyr Leu	
70 75 80	
AAC ATT TGG GTG CCC CAG GGC AGG AAG CAA GTC TCC CGG GAC CTG CCC	447
Asn Ile Trp Val Pro Gln Gly Arg Lys Gln Val Ser Arg Asp Leu Pro	
85 90 95	
GTT ATG ATC TGG ATC TAT GGA GGC GCC TTC CTC ATG GGG TCC GGC CAT	495
Val Met Ile Trp Ile Tyr Gly Gly Ala Phe Leu Met Gly Ser Gly His	
100 105 110 115	

GGG GCC AAC TTC CTC AAC AAC TAC CTG TAT GAC GGC GAG GAG ATC GCC Gly Ala Asn Phe Leu Asn Asn Tyr Leu Tyr Asp Gly Glu Glu Ile Ala 120 125 130	543
ACA CGC GGA AAC GTC ATC GTG GTC ACC TTC AAC TAC CGT GTC GGC CCC Thr Arg Gly Asn Val Ile Val Val Thr Phe Asn Tyr Arg Val Gly Pro 135 140 145	591
CTT GGG TTC CTC AGC ACT GGG GAC GCC AAT CTG CCA GGT AAC TAT GGC Leu Gly Phe Leu Ser Thr Gly Ala Asn Leu Pro Gly Asn Tyr Gly 150 155 160	639
CTT CGG GAT CAG CAC ATG GCC ATT GCT TGG GTG AAG AGG AAT ATC GCG Leu Arg Asp Gln His Met Ala Ile Ala Trp Val Lys Arg Asn Ile Ala 165 170 175	687
GCC TTC GGG GGG GAC CCC AAC AAC ATC ACG CTC TTC GGG GAG TCT GCT Ala Phe Gly Gly Asp Pro Asn Asn Ile Thr Leu Phe Gly Glu Ser Ala 180 185 190 195	735
GGA GGT GCC AGC GTC TCT CTG CAG ACC CTC TCC CCC TAC AAC AAG GGC Gly Gly Ala Ser Val Ser Leu Gln Thr Leu Ser Pro Tyr Asn Lys Gly 200 205 210	783
CTC ATC CGG CGA GCC ATC AGC CAG AGC GGC GTG GCC CTG AGT CCC TGG Leu Ile Arg Arg Ala Ile Ser Gln Ser Gly Val Ala Leu Ser Pro Trp 215 220 225	831
GTC ATC CAG AAA AAC CCA CTC TTC TGG GCC AAA AAG GTG GCT GAG AAG Val Ile Gln Lys Asn Pro Leu Phe Trp Ala Lys Lys Val Ala Glu Lys 230 235 240	879
GTG GGT TGC CCT GTG GGT GAT GCC GCC AGG ATG GCC CAG TGT CTG AAG Val Gly Cys Pro Val Gly Asp Ala Ala Arg Met Ala Gln Cys Leu Lys 245 250 255	927
GTT ACT GAT CCC CGA GCC CTG ACG CTG GCC TAT AAG GTG CCG CTG GCA Val Thr Asp Pro Arg Ala Leu Thr Leu Ala Tyr Lys Val Pro Leu Ala 260 265 270 275	975
GGC CTG GAG TAC CCC ATG CTG CAC TAT GTG GGC TTC GTC CCT GTC ATT Gly Leu Glu Tyr Pro Met Leu His Tyr Val Gly Phe Val Pro Val Ile 280 285 290	1023
GAT GGA GAC TTC ATC CCC GCT GAC CCG ATC AAC CTG TAC GCC AAC GCC Asp Gly Asp Phe Ile Pro Ala Asp Pro Ile Asn Leu Tyr Ala Asn Ala 295 300 305	1071
GCC GAC ATC GAC TAT ATA GCA GGC ACC AAC AAC ATG GAC GGC CAC ATC Ala Asp Ile Asp Tyr Ile Ala Gly Thr Asn Asn Met Asp Gly His Ile 310 315 320	1119
TTC GCC AGC ATC GAC ATG CCT GCC ATC AAC AAG GGC AAC AAG AAA GTC Phe Ala Ser Ile Asp Met Pro Ala Ile Asn Lys Gly Asn Lys Lys Val 325 330 335	1167
ACG GAG GAG GAC TTC TAC AAG CTG GTC AGT GAG TTC ACA ATC ACC AAG Thr Glu Glu Asp Phe Tyr Lys Leu Val Ser Glu Phe Thr Ile Thr Lys 340 345 350 355	1215
GGG CTC AGA GGC GCC AAG ACG ACC TTT GAT GTC TAC ACC GAG TCC TGG Gly Leu Arg Gly Ala Lys Thr Thr Phe Asp Val Tyr Thr Glu Ser Trp 360 365 370	1263
GCC CAG GAC CCA TCC CAG GAG AAT AAG AAG AAG ACT GTG GTG GAC TTT Ala Gln Asp Pro Ser Gln Glu Asn Lys Lys Lys Thr Val Val Asp Phe 375 380 385	1311

GAG ACC GAT GTC CTC TTC CTG GTG CCC ACC GAG ATT GCC CTA GCC CAG Glu Thr Asp Val Leu Phe Leu Val Pro Thr Glu Ile Ala Leu Ala Gln 390 395 400	1359
CAC AGA GCC AAT GCC AAG AGT GCC AAG ACC TAC GCC TAC CTG TTT TCC His Arg Ala Asn Ala Lys Ser Ala Lys Thr Tyr Ala Tyr Leu Phe Ser 405 410 415	1407
CAT CCC TCT CGG ATG CCC GTC TAC CCC AAA TGG GTG GGG GCC GAC CAT His Pro Ser Arg Met Pro Val Tyr Pro Lys Trp Val Gly Ala Asp His 420 425 430 435	1455
GCA GAT GAC ATT CAG TAC GTT TTC GGG AAG CCC TTC GCC ACC CCC ACG Ala Asp Asp Ile Gln Tyr Val Phe Gly Lys Pro Phe Ala Thr Pro Thr 440 445 450	1503
GGC TAC CGG CCC CAA GAC AGG ACA GTC TCT AAG GCC ATG ATC GCC TAC Gly Tyr Arg Pro Gln Asp Arg Thr Val Ser Lys Ala Met Ile Ala Tyr 455 460 465	1551
TGG ACC AAC TTT GCC AAA ACA GGG GAC CCC AAC ATG GGC GAC TCG GCT Trp Thr Asn Phe Ala Lys Thr Gly Asp Pro Asn Met Gly Asp Ser Ala 470 475 480	1599
GTG CCC ACA CAC TGG GAA CCC TAC ACT ACG GAA AAC AGC GGC TAC CTG Val Pro Thr His Trp Glu Pro Tyr Thr Thr Glu Asn Ser Gly Tyr Leu 485 490 495	1647
GAG ATC ACC AAG AAG ATG GGC AGC AGC TCC ATG AAG GCG AGC CTG AGA Glu Ile Thr Lys Lys Met Gly Ser Ser Ser Met Lys Arg Ser Leu Arg 500 505 510 515	1695
ACC AAC TTC CTG CGC TAC TGG ACC CTC ACC TAT CTG GCG CTG CCC ACA Thr Asn Phe Leu Arg Tyr Trp Thr Leu Thr Tyr Leu Ala Leu Pro Thr 520 525 530	1743
GTG ACC GAC CAG GAG GCC ACC CCT GTG CCC CCC ACA GCG GAC TCC GAG Val Thr Asp Gln Glu Ala Thr Pro Val Pro Pro Thr Gly Asp Ser Glu 535 540 545	1791
GCC ACT CCC GTG CCC CCC ACG GGT GAC TCC GAG ACC GCG CCC GTG CCG Ala Thr Pro Val Pro Pro Thr Gly Asp Ser Glu Thr Ala Pro Val Pro 550 555 560	1839
CCC ACG GGT GAC TCC GGG GCC CCC CCC GTG CCG CCC ACG GGT GAC TCC Pro Thr Gly Asp Ser Gly Ala Pro Pro Val Pro Pro Thr Gly Asp Ser 565 570 575	1887
GGG GCC CCC CCC GTG CCG CCC ACG GGT GAC TCC GGG GCG CCC CCC GTG Gly Ala Pro Pro Val Pro Pro Thr Gly Asp Ser Gly Ala Pro Pro Val 580 585 590 595	1935
CCG CCC ACG GGT GAC TCC GGG GCC CCC CCC GTG CCG CCC ACG GGT GAC Pro Pro Thr Gly Asp Ser Gly Ala Pro Pro Val Pro Pro Thr Gly Asp 600 605 610	1983
TCC GGG GCC CCC CCC GTG CCG CCC ACG GGT GAC TCC GGG GCC CCC CCC Ser Gly Ala Pro Pro Val Pro Pro Thr Gly Asp Ser Gly Ala Pro Pro 615 620 625	2031
GTG CCG CCC ACG GGT GAC TCC GGC GCC CCC CCC GTG CCG CCC ACG GGT Val Pro Pro Thr Gly Asp Ser Gly Ala Pro Pro Val Pro Pro Thr Gly 630 635 640	2079
GAC GCC GGG CCC CCC CCC GTG CCG CCC ACG GGT GAC TCC GGC GCC CCC Asp Ala Gly Pro Pro Pro Val Pro Pro Thr Gly Asp Ser Gly Ala Pro 645 650 655	2127

```

CCC GTG CCG CCC ACG GGT GAC TCC GGG GCC CCC CCC GTG ACC CCC ACG      2175
Pro Val Pro Pro Thr Gly Asp Ser Gly Ala Pro Pro Val Thr Pro Thr
660                               665                               670       675

GGT GAC TCC GAG ACC GCC CCC GTG CCG CCC ACG GGT GAC TCC GGG GCC      2223
Gly Asp Ser Glu Thr Ala Pro Val Pro Pro Thr Gly Asp Ser Gly Ala
680                               685                               690

CCC CCT GTG CCC CCC ACG GGT GAC TCT GAG GCT GCC CCT GTG CCC CCC      2271
Pro Pro Val Pro Pro Thr Gly Asp Ser Glu Ala Ala Pro Val Pro Pro
695                               700                               705

ACA GAT GAC TCC AAG GAA GCT CAG ATG CCT GCA GTC ATT AGG TTT TAG      2319
Thr Asp Asp Ser Lys Glu Ala Gln Met Pro Ala Val Ile Arg Phe *
710                               715                               720

CGTCCCATGA GCCTTGAT CAAGAGGCCA CAAGAGTGGG ACCCCAGGGG CTCCCCTCCC      2379

ATCTTGAGCT CTTCCTGAAT AAAGCCTCAT ACCCCTAAAA AAAAAAAAAA      2428

```

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 746 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

Met Leu Thr Met Gly Arg Leu Gln Leu Val Val Leu Gly Leu Thr Cys
-23          -20          -15          -10

Cys Trp Ala Val Ala Ser Ala Ala Lys Leu Gly Ala Val Tyr Thr Glu
-5          1          5

Gly Gly Phe Val Glu Gly Val Asn Lys Lys Leu Gly Leu Leu Gly Asp
10          15          20          25

Ser Val Asp Ile Phe Lys Gly Ile Pro Phe Ala Ala Pro Thr Lys Ala
30          35          40

Leu Glu Asn Pro Gln Pro His Pro Gly Trp Gln Gly Thr Leu Lys Ala
45          50          55

Lys Asn Phe Lys Lys Arg Cys Leu Gln Ala Thr Ile Thr Gln Asp Ser
60          65          70

Thr Tyr Gly Asp Glu Asp Cys Leu Tyr Leu Asn Ile Trp Val Pro Gln
75          80          85

Gly Arg Lys Gln Val Ser Arg Asp Leu Pro Val Met Ile Trp Ile Tyr
90          95          100          105

Gly Gly Ala Phe Leu Met Gly Ser Gly His Gly Ala Asn Phe Leu Asn
110          115          120

Asn Tyr Leu Tyr Asp Gly Glu Glu Ile Ala Thr Arg Gly Asn Val Ile
125          130          135

Val Val Thr Phe Asn Tyr Arg Val Gly Pro Leu Gly Phe Leu Ser Thr
140          145          150

Gly Asp Ala Asn Leu Pro Gly Asn Tyr Gly Leu Arg Asp Gln His Met
155          160          165

```

Ala Ile Ala Trp Val Lys Arg Asn Ile Ala Ala Phe Gly Gly Asp Pro
 170 175 180 185
 Asn Asn Ile Thr Leu Phe Gly Glu Ser Ala Gly Gly Ala Ser Val Ser
 190 195 200
 Leu Gln Thr Leu Ser Pro Tyr Asn Lys Gly Leu Ile Arg Arg Ala Ile
 205 210 215
 Ser Gln Ser Gly Val Ala Leu Ser Pro Trp Val Ile Gln Lys Asn Pro
 220 225 230
 Leu Phe Trp Ala Lys Lys Val Ala Glu Lys Val Gly Cys Pro Val Gly
 235 240 245
 Asp Ala Ala Arg Met Ala Gln Cys Leu Lys Val Thr Asp Pro Arg Ala
 250 255 260 265
 Leu Thr Leu Ala Tyr Lys Val Pro Leu Ala Gly Leu Glu Tyr Pro Met
 270 275 280
 Leu His Tyr Val Gly Phe Val Pro Val Ile Asp Gly Asp Phe Ile Pro
 285 290 295
 Ala Asp Pro Ile Asn Leu Tyr Ala Asn Ala Ala Asp Ile Asp Tyr Ile
 300 305 310
 Ala Gly Thr Asn Asn Met Asp Gly His Ile Phe Ala Ser Ile Asp Met
 315 320 325
 Pro Ala Ile Asn Lys Gly Asn Lys Lys Val Thr Glu Glu Asp Phe Tyr
 330 335 340 345
 Lys Leu Val Ser Glu Phe Thr Ile Thr Lys Gly Leu Arg Gly Ala Lys
 350 355 360
 Thr Thr Phe Asp Val Tyr Thr Glu Ser Trp Ala Gln Asp Pro Ser Gln
 365 370 375
 Glu Asn Lys Lys Lys Thr Val Val Asp Phe Glu Thr Asp Val Leu Phe
 380 385 390
 Leu Val Pro Thr Glu Ile Ala Leu Ala Gln His Arg Ala Asn Ala Lys
 395 400 405
 Ser Ala Lys Thr Tyr Ala Tyr Leu Phe Ser His Pro Ser Arg Met Pro
 410 415 420 425
 Val Tyr Pro Lys Trp Val Gly Ala Asp His Ala Asp Asp Ile Gln Tyr
 430 435 440
 Val Phe Gly Lys Pro Phe Ala Thr Pro Thr Gly Tyr Arg Pro Gln Asp
 445 450 455
 Arg Thr Val Ser Lys Ala Met Ile Ala Tyr Trp Thr Asn Phe Ala Lys
 460 465 470
 Thr Gly Asp Pro Asn Met Gly Asp Ser Ala Val Pro Thr His Trp Glu
 475 480 485
 Pro Tyr Thr Thr Glu Asn Ser Gly Tyr Leu Glu Ile Thr Lys Lys Met
 490 495 500 505
 Gly Ser Ser Ser Met Lys Arg Ser Leu Arg Thr Asn Phe Leu Arg Tyr
 510 515 520
 Trp Thr Leu Thr Tyr Leu Ala Leu Pro Thr Val Thr Asp Gln Glu Ala
 525 530 535

Thr Pro Val Pro Pro Thr Gly Asp Ser Glu Ala Thr Pro Val Pro Pro
 540 545 550
 Thr Gly Asp Ser Glu Thr Ala Pro Val Pro Pro Thr Gly Asp Ser Gly
 555 560 565
 Ala Pro Pro Val Pro Pro Thr Gly Asp Ser Gly Ala Pro Pro Val Pro
 570 575 580 585
 Pro Thr Gly Asp Ser Gly Ala Pro Pro Val Pro Pro Thr Gly Asp Ser
 590 595 600
 Gly Ala Pro Pro Val Pro Pro Thr Gly Asp Ser Gly Ala Pro Pro Val
 605 610 615
 Pro Pro Thr Gly Asp Ser Gly Ala Pro Pro Val Pro Pro Thr Gly Asp
 620 625 630
 Ser Gly Ala Pro Pro Val Pro Pro Thr Gly Asp Ala Gly Pro Pro Pro
 635 640 645
 Val Pro Pro Thr Gly Asp Ser Gly Ala Pro Pro Val Pro Pro Thr Gly
 650 655 660 665
 Asp Ser Gly Ala Pro Pro Val Thr Pro Thr Gly Asp Ser Glu Thr Ala
 670 675 680
 Pro Val Pro Pro Thr Gly Asp Ser Gly Ala Pro Pro Val Pro Pro Thr
 685 690 695
 Gly Asp Ser Glu Ala Ala Pro Val Pro Pro Thr Asp Asp Ser Lys Glu
 700 705 710
 Ala Gln Met Pro Ala Val Ile Arg Phe *
 715 720

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 722 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (F) TISSUE TYPE: Mammary gland

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Ala Lys Leu Gly Ala Val Tyr Thr Glu Gly Gly Phe Val Glu Gly Val
 1 5 10 15
 Asn Lys Lys Leu Gly Leu Leu Gly Asp Ser Val Asp Ile Phe Lys Gly
 20 25 30
 Ile Pro Phe Ala Ala Pro Thr Lys Ala Leu Glu Asn Pro Gln Pro His
 35 40 45
 Pro Gly Trp Gln Gly Thr Leu Lys Ala Lys Asn Phe Lys Lys Arg Cys
 50 55 60

Leu Gln Ala Thr Ile Thr Gln Asp Ser Thr Tyr Gly Asp Glu Asp Cys
 65 70 75 80
 Leu Tyr Leu Asn Ile Trp Val Pro Gln Gly Arg Lys Gln Val Ser Arg
 85 90 95
 Asp Leu Pro Val Met Ile Trp Ile Tyr Gly Gly Ala Phe Leu Met Gly
 100 105 110
 Ser Gly His Gly Ala Asn Phe Leu Asn Asn Tyr Leu Tyr Asp Gly Glu
 115 120 125
 Glu Ile Ala Thr Arg Gly Asn Val Ile Val Val Thr Phe Asn Tyr Arg
 130 135 140
 Val Gly Pro Leu Gly Phe Leu Ser Thr Gly Asp Ala Asn Leu Pro Gly
 145 150 155 160
 Asn Tyr Gly Leu Arg Asp Gln His Met Ala Ile Ala Trp Val Lys Arg
 165 170 175
 Asn Ile Ala Ala Phe Gly Gly Asp Pro Asn Asn Ile Thr Leu Phe Gly
 180 185 190
 Glu Ser Ala Gly Gly Ala Ser Val Ser Leu Gln Thr Leu Ser Pro Tyr
 195 200 205
 Asn Lys Gly Leu Ile Arg Arg Ala Ile Ser Gln Ser Gly Val Ala Leu
 210 215 220
 Ser Pro Trp Val Ile Gln Lys Asn Pro Leu Phe Trp Ala Lys Lys Val
 225 230 235 240
 Ala Glu Lys Val Gly Cys Pro Val Gly Asp Ala Ala Arg Met Ala Gln
 245 250 255
 Cys Leu Lys Val Thr Asp Pro Arg Ala Leu Thr Leu Ala Tyr Lys Val
 260 265 270
 Pro Leu Ala Gly Leu Glu Tyr Pro Met Leu His Tyr Val Gly Phe Val
 275 280 285
 Pro Val Ile Asp Gly Asp Phe Ile Pro Ala Asp Pro Ile Asn Leu Tyr
 290 295 300
 Ala Asn Ala Ala Asp Ile Asp Tyr Ile Ala Gly Thr Asn Asn Met Asp
 305 310 315 320
 Gly His Ile Phe Ala Ser Ile Asp Met Pro Ala Ile Asn Lys Gly Asn
 325 330 335
 Lys Lys Val Thr Glu Glu Asp Phe Tyr Lys Leu Val Ser Glu Phe Thr
 340 345 350
 Ile Thr Lys Gly Leu Arg Gly Ala Lys Thr Thr Phe Asp Val Tyr Thr
 355 360 365
 Glu Ser Trp Ala Gln Asp Pro Ser Gln Glu Asn Lys Lys Lys Thr Val
 370 375 380
 Val Asp Phe Glu Thr Asp Val Leu Phe Leu Val Pro Thr Glu Ile Ala
 385 390 395 400
 Leu Ala Gln His Arg Ala Asn Ala Lys Ser Ala Lys Thr Tyr Ala Tyr
 405 410 415
 Leu Phe Ser His Pro Ser Arg Met Pro Val Tyr Pro Lys Trp Val Gly
 420 425 430

Ala Asp His Ala Asp Asp Ile Gln Tyr Val Phe Gly Lys Pro Phe Ala
 435 440 445
 Thr Pro Thr Gly Tyr Arg Pro Gln Asp Arg Thr Val Ser Lys Ala Met
 450 455 460
 Ile Ala Tyr Trp Thr Asn Phe Ala Lys Thr Gly Asp Pro Asn Met Gly
 465 470 475 480
 Asp Ser Ala Val Pro Thr His Trp Glu Pro Tyr Thr Thr Glu Asn Ser
 485 490 495
 Gly Tyr Leu Glu Ile Thr Lys Lys Met Gly Ser Ser Ser Met Lys Arg
 500 505 510
 Ser Leu Arg Thr Asn Phe Leu Arg Tyr Trp Thr Leu Thr Tyr Leu Ala
 515 520 525
 Leu Pro Thr Val Thr Asp Gln Glu Ala Thr Pro Val Pro Pro Thr Gly
 530 535 540
 Asp Ser Glu Ala Thr Pro Val Pro Pro Thr Gly Asp Ser Glu Thr Ala
 545 550 555 560
 Pro Val Pro Pro Thr Gly Asp Ser Gly Ala Pro Pro Val Pro Pro Thr
 565 570 575
 Gly Asp Ser Gly Ala Pro Pro Val Pro Pro Thr Gly Asp Ser Gly Ala
 580 585 590
 Pro Pro Val Pro Pro Thr Gly Asp Ser Gly Ala Pro Pro Val Pro Pro
 595 600 605
 Thr Gly Asp Ser Gly Ala Pro Pro Val Pro Pro Thr Gly Asp Ser Gly
 610 615 620
 Ala Pro Pro Val Pro Pro Thr Gly Asp Ser Gly Ala Pro Pro Val Pro
 625 630 635 640
 Pro Thr Gly Asp Ala Gly Pro Pro Pro Val Pro Pro Thr Gly Asp Ser
 645 650 655
 Gly Ala Pro Pro Val Pro Pro Thr Gly Asp Ser Gly Ala Pro Pro Val
 660 665 670
 Thr Pro Thr Gly Asp Ser Glu Thr Ala Pro Val Pro Pro Thr Gly Asp
 675 680 685
 Ser Gly Ala Pro Pro Val Pro Pro Thr Gly Asp Ser Glu Ala Ala Pro
 690 695 700
 Val Pro Pro Thr Asp Asp Ser Lys Glu Ala Gln Met Pro Ala Val Ile
 705 710 715 720
 Arg Phe

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 568 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens
(F) TISSUE TYPE: Mammary gland

(ix) FEATURE:

(A) NAME/KEY: Peptide
(B) LOCATION: 1..568
(D) OTHER INFORMATION: /label= Variant_C

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Hansson, Lennart
Blackberg, Lars
Edlund, Michael
Lundberg, Lennart
Stromqvist, Mats
Hernell, Olle
(B) TITLE: Recombinant Human Milk Bile Salt-stimulated
Lipase
(C) JOURNAL: J. Biol. Chem.
(D) VOLUME: 268
(E) ISSUE: 35
(F) PAGES: 26692-26698
(G) DATE: Dec. 15-1993

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Ala	Lys	Leu	Gly	Ala	Val	Tyr	Thr	Glu	Gly	Gly	Phe	Val	Glu	Gly	Val	1	5	10	15
Asn	Lys	Lys	Leu	Gly	Leu	Leu	Gly	Asp	Ser	Val	Asp	Ile	Phe	Lys	Gly	20	25	30	
Ile	Pro	Phe	Ala	Ala	Pro	Thr	Lys	Ala	Leu	Glu	Asn	Pro	Gln	Pro	His	35	40	45	
Pro	Gly	Trp	Gln	Gly	Thr	Leu	Lys	Ala	Lys	Asn	Phe	Lys	Lys	Arg	Cys	50	55	60	
Leu	Gln	Ala	Thr	Ile	Thr	Gln	Asp	Ser	Thr	Tyr	Gly	Asp	Glu	Asp	Cys	65	70	75	80
Leu	Tyr	Leu	Asn	Ile	Trp	Val	Pro	Gln	Gly	Arg	Lys	Gln	Val	Ser	Arg	85	90	95	
Asp	Leu	Pro	Val	Met	Ile	Trp	Ile	Tyr	Gly	Gly	Ala	Phe	Leu	Met	Gly	100	105	110	
Ser	Gly	His	Gly	Ala	Asn	Phe	Leu	Asn	Asn	Tyr	Leu	Tyr	Asp	Gly	Glu	115	120	125	
Glu	Ile	Ala	Thr	Arg	Gly	Asn	Val	Ile	Val	Val	Thr	Phe	Asn	Tyr	Arg	130	135	140	
Val	Gly	Pro	Leu	Gly	Phe	Leu	Ser	Thr	Gly	Asp	Ala	Asn	Leu	Pro	Gly	145	150	155	160
Asn	Tyr	Gly	Leu	Arg	Asp	Gln	His	Met	Ala	Ile	Ala	Trp	Val	Lys	Arg	165	170	175	
Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asp	Pro	Asn	Asn	Ile	Thr	Leu	Phe	Gly	180	185	190	
Glu	Ser	Ala	Gly	Gly	Ala	Ser	Val	Ser	Leu	Gln	Thr	Leu	Ser	Pro	Tyr	195	200	205	

Asn Lys Gly Leu Ile Arg Arg Ala Ile Ser Gln Ser Gly Val Ala Leu
 210 215 220
 Ser Pro Trp Val Ile Gln Lys Asn Pro Leu Phe Trp Ala Lys Lys Val
 225 230 235 240
 Ala Glu Lys Val Gly Cys Pro Val Gly Asp Ala Ala Arg Met Ala Gln
 245 250 255
 Cys Leu Lys Val Thr Asp Pro Arg Ala Leu Thr Leu Ala Tyr Lys Val
 260 265 270
 Pro Leu Ala Gly Leu Glu Tyr Pro Met Leu His Tyr Val Gly Phe Val
 275 280 285
 Pro Val Ile Asp Gly Asp Phe Ile Pro Ala Asp Pro Ile Asn Leu Tyr
 290 295 300
 Ala Asn Ala Ala Asp Ile Asp Tyr Ile Ala Gly Thr Asn Asn Met Asp
 305 310 315 320
 Gly His Ile Phe Ala Ser Ile Asp Met Pro Ala Ile Asn Lys Gly Asn
 325 330 335
 Lys Lys Val Thr Glu Glu Asp Phe Tyr Lys Leu Val Ser Glu Phe Thr
 340 345 350
 Ile Thr Lys Gly Leu Arg Gly Ala Lys Thr Thr Phe Asp Val Tyr Thr
 355 360 365
 Glu Ser Trp Ala Gln Asp Pro Ser Gln Glu Asn Lys Lys Lys Thr Val
 370 375 380
 Val Asp Phe Glu Thr Asp Val Leu Phe Leu Val Pro Thr Glu Ile Ala
 385 390 395 400
 Leu Ala Gln His Arg Ala Asn Ala Lys Ser Ala Lys Thr Tyr Ala Tyr
 405 410 415
 Leu Phe Ser His Pro Ser Arg Met Pro Val Tyr Pro Lys Trp Val Gly
 420 425 430
 Ala Asp His Ala Asp Asp Ile Gln Tyr Val Phe Gly Lys Pro Phe Ala
 435 440 445
 Thr Pro Thr Gly Tyr Arg Pro Gln Asp Arg Thr Val Ser Lys Ala Met
 450 455 460
 Ile Ala Tyr Trp Thr Asn Phe Ala Lys Thr Gly Asp Pro Asn Met Gly
 465 470 475 480
 Asp Ser Ala Val Pro Thr His Trp Glu Pro Tyr Thr Thr Glu Asn Ser
 485 490 495
 Gly Tyr Leu Glu Ile Thr Lys Lys Met Gly Ser Ser Ser Met Lys Arg
 500 505 510
 Ser Leu Arg Thr Asn Phe Leu Arg Tyr Trp Thr Leu Thr Tyr Leu Ala
 515 520 525
 Leu Pro Thr Val Thr Asp Gln Gly Ala Pro Pro Val Pro Pro Thr Gly
 530 535 540
 Asp Ser Gly Ala Pro Pro Val Pro Pro Thr Gly Asp Ser Lys Glu Ala
 545 550 555 560
 Gln Met Pro Ala Val Ile Arg Phe
 565

Applicant's or agent's file
reference number

H:

58-1 WO

International applicat

No.

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>9</u> , line <u>8</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution The National Collections of Industrial and Marine Bacteria Limited (NCIMB)	
Address of depositary institution (including postal code and country) 23 St Machar Drive Aberdeen AB2 1RY Scotland, UK	
Date of deposit 2 May 1995	Accession Number NCIMB 40721
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
In respect of all designated states in which such action is possible and to the extent that it is legally permissible under the law of the designated state, it is requested that a sample of the deposited micro-organism be made available only by the issue thereof to an independent expert, in accordance with the relevant patent legislation, e.g. Rule 28(4) EPC, and generally similar provisions <i>mutatis mutandis</i> for any other designated state.	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	

For receiving Office use only <input type="checkbox"/> This sheet was received with the international application Authorized officer	For International Bureau use only <input type="checkbox"/> This sheet was received by the International Bureau on: Authorized officer
--	---

Applicant's or agent's file reference number H: 5P-1 WO	International application No.
---	-------------------------------

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>12</u> , line <u>19-20</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution The National Collections of Industrial and Marine Bacteria Limited (NCIMB)	
Address of depositary institution (including postal code and country) 23 St Machar Drive Aberdeen AB2 1RY Scotland, UK	
Date of deposit 2 May 1995	Accession Number NCIMB 40723
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
In respect of all designated states in which such action is possible and to the extent that it is legally permissible under the law of the designated state, it is requested that a sample of the deposited micro-organism be made available only by the issue thereof to an independent expert, in accordance with the relevant patent legislation, e.g. Rule 28(4) EPC, and generally similar provisions <i>mutatis mutandis</i> for any other designated state.	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	
For receiving Office use only <input type="checkbox"/> This sheet was received with the international application Authorized officer	For International Bureau use only <input type="checkbox"/> This sheet was received by the International Bureau on: Authorized officer

Applicant's or agent's file reference number	H 258-1 WO	International applicant	No
---	------------	-------------------------	----

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>17</u> , line <u>18-19</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution The National Collections of Industrial and Marine Bacteria Limited (NCIMB)	
Address of depositary institution (including postal code and country) 23 St Machar Drive Aberdeen AB2 1RY Scotland, UK	
Date of deposit 2 May 1995	Accession Number NCIMB 40722
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
<p>In respect of all designated states in which such action is possible and to the extent that it is legally permissible under the law of the designated state, it is requested that a sample of the deposited micro-organism be made available only by the issue thereof to an independent expert, in accordance with the relevant patent legislation, e.g. Rule 28(4) EPC, and generally similar provisions <i>mutatis mutandis</i> for any other designated state.</p>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	

<p>For receiving Office use only</p> <p><input type="checkbox"/> This sheet was received with the international application</p> <p>Authorized officer</p>	<p>For International Bureau use only</p> <p><input type="checkbox"/> This sheet was received by the International Bureau on:</p> <p>Authorized officer</p>
---	--